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Pro  Arg  Ser  Pro  Gly  Pro  Val  Pro  His  Pro  Ala  Gln  Ser  Lys  Ala  Thr
                20                        25                30

Glu  Ala  Gly  Gly  Gly  Asn  Pro  Ser  Gly  Ile  Tyr  Ser  Ala  Ile  Ile  Ser
                35                        40                45

Arg  Asn  Phe  Pro  Ile  Ile  Gly  Val  Lys  Glu  Lys  Thr  Phe  Glu  Gln  Leu
  50                        55                    60

His  Lys  Lys  Cys  Leu  Glu  Lys  Lys  Val  Leu  Tyr  Val  Asp  Pro  Glu  Phe
  65                        70                    75                80

Pro  Pro  Asp  Glu  Thr  Ser  Leu  Phe  Tyr  Ser  Gln  Lys  Phe  Pro  Ile  Gln
                85                        90                95

Phe  Val  Trp  Lys  Arg  Pro  Pro  Glu  Ile  Cys  Glu  Asn  Pro  Arg  Phe  Ile
                100                       105                110

Ile  Asp  Gly  Ala  Asn  Arg  Thr  Asp  Ile  Cys  Gln  Gly  Glu  Leu  Gly  Asp
                115                       120                125

Cys  Trp  Phe  Leu  Ala  Ala  Ile  Ala  Cys  Leu  Thr  Leu  Asn  Gln  His  Leu
  130                        135                    140

Leu  Phe  Arg  Val  Ile  Pro  His  Asp  Gln  Ser  Phe  Ile  Glu  Asn  Tyr  Ala
  145                        150                    155                160

Gly  Ile  Phe  His  Phe  Gln  Phe  Trp  Arg  Tyr  Gly  Glu  Trp  Val  Asp  Val
                165                        170                175

Val  Ile  Asp  Asp  Cys  Leu  Pro  Thr  Tyr  Asn  Asn  Gln  Leu  Val  Phe  Thr
                180                        185                190

Lys  Ser  Asn  His  Arg  Asn  Glu  Phe  Trp  Ser  Ala  Leu  Leu  Glu  Lys  Ala
  195                        200                    205

Tyr  Ala  Lys  Leu  His  Gly  Ser  Tyr  Glu  Ala  Leu  Lys  Gly  Gly  Asn  Thr
  210                        215                    220

Thr  Glu  Ala  Met  Glu  Asp  Phe  Thr  Gly  Gly  Val  Ala  Glu  Phe  Phe  Glu
  225                        230                    235                240

Ile  Arg  Asp  Ala  Pro  Ser  Asp  Met  Tyr  Lys  Ile  Met  Lys  Lys  Ala  Ile
                245                        250                255

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Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
 260 265 270
 Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Ala
 275 280 285
 Arg Met Val Arg Asn Met Asp Asn Ser Leu Leu Gln Asp Ser Asp Leu
 290 295 300
 Asp Pro Arg Gly Ser Asp Glu Arg Pro Thr Arg Thr Ile Ile Pro Val
 305 310 315 320
 Gln Tyr Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
 325 330 335
 Ser Val Thr Gly Leu Asp Glu Val Pro Phe Lys Gly Glu Lys Val Lys
 340 345 350
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
 355 360 365
 Trp Ser Asp Arg Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
 370 375 380
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
 385 390 395 400
 Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
 405 410 415
 Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
 420 425 430
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
 435 440 445
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
 450 455 460
 Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
 465 470 475 480
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
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 Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
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 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
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Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
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 Lys Arg Asn Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
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 Lys Gly Lys Thr Ser Pro Asp Lys Gln Lys Gln Ser Pro Gln Pro Gln
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 Pro Gly Ser Ser Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
 645 650 655
 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
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 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
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 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
 705 710 715 720
 Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
 725 730 735
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
 755 760 765
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
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 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
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 Leu Thr Met Tyr Ala
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 Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Gly Lys Thr Thr
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 Glu Ala Gly Gly Gly His Pro Gly Gly Ile Tyr Ser Ala Ile Ile Ser
 35 40 45
 Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
 50 55 60
 His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Leu Asp Pro Glu Phe
 65 70 75 80
 Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
 85 90 95
 Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
 100 105 110
 Ile Gly Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Asp Leu Gly Asp
 115 120 125
 Cys Trp Leu Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Glu Arg Leu
 130 135 140

Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Thr Glu Asn Tyr Ala
 145 150 155 160
 Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Asp Trp Val Asp Val
 165 170 175
 Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
 180 185 190
 Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
 195 200 205
 Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
 210 215 220
 Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Thr Glu Phe Phe Glu
 225 230 235 240
 Ile Lys Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Arg Lys Ala Ile
 245 250 255
 Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
 260 265 270
 Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Ala
 275 280 285
 Arg Met Val Arg Asn Met Asp Asn Ser Leu Leu Arg Asp Ser Asp Leu
 290 295 300
 Asp Pro Arg Ala Ser Asp Asp Arg Pro Ser Arg Thr Ile Val Pro Val
 305 310 315 320
 Gln Tyr Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
 325 330 335
 Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
 340 345 350
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
 355 360 365
 Trp Ser Asp Gly Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
 370 375 380
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
 385 390 395 400
 Tyr Asp Asp Phe Val Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
 405 410 415
 Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
 420 425 430
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
 435 440 445

Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
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 Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
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 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
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 Lys Arg Asn Leu Ser Glu Glu Ala Glu Asn Thr Ile Ser Val Asp Arg
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 Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ala Glu Glu Gly
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 Pro Gly His Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
 645 650 655
 Ile Phe Arg Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
 660 665 670
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 Thr Gln Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
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 740 745 750

Asp Ala Gly Phe His Leu Asn Ser Gln Leu Tyr Asp Ile Ile Thr Met
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 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
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Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser
 35 40 45

Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
 50 55 60

His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
 65 70 75 80

Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
 85 90 95

Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
 100 105 110

Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
 115 120 125

Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
 130 135 140

Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
 145 150 155 160

Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
 165 170 175

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
 180 185 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
 195 200 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
 210 215 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
 225 230 235 240

Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
 245 250 255

Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
 260 265 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Asp Leu Ile Ala
 275 280 285

Arg Met Val Arg Asn Met Glu Asn Ser Arg Leu Arg Asp Ser Ile Leu
 290 295 300

Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Thr Ile Val Pro Val
 305 310 315 320

Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
 325 330 335

Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
 340 345 350
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
 355 360 365
 Trp Ser Asp Ser Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
 370 375 380
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
 385 390 395 400
 Tyr Asp Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
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 Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
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 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Thr Gly Arg
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 Lys Arg Lys Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
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 625 630 635 640

Pro Ser Asn Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
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 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
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 Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
 675 680 685
 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
 690 695 700
 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
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 725 730 735
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
 755 760 765
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
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 35 40 45
 Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
 50 55 60
 His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
 65 70 75 80
 Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
 85 90 95
 Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
 100 105 110
 Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
 115 120 125
 Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
 130 135 140
 Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
 145 150 155 160
 Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
 165 170 175
 Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
 180 185 190
 Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
 195 200 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
 210 215 220
 Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
 225 230 235 240
 Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
 245 250 255
 Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
 260 265 270
 Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Glu
 275 280 285
 Arg Met Val Arg Asn Met Asp Asn Ser Arg Leu Arg Asp Ser Ile Leu
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 Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Met Ile Val Pro Val
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 Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
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 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
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 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
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 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
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 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
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 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
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 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
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Leu Thr Met Tyr Ala
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<210> 16
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<210> 17
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<210> 19
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<223> /label= Table 3

<400> 19
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<210> 20
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<400> 20
ctttccttga aggtagctgt at                             22

<210> 21
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<400> 21
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<210> 22
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actccgtctc aaaaaaatac ct
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<210> 23
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<223> /label= Table 3

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<210> 24
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<210> 27
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<210> 28
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<223> /label= Table 3

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<220>
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<222> (1)..(21)
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<210> 32
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<210> 39
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 <223> /label= Table 3

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19

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<220>
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21

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<220>
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<210> 44
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<223> /label= Table 3

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<210> 46
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<220>
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<220>
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<223> /label= Table 3

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<223> /label= Table 3

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<220>
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<223> /label= Table 3

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<220>
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<222> (1)..(21)
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21

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20

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<220>
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<222> (1)..(19)
<223> /label= Table 3

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<220> <221> misc_feature <222> (1)..(20) <223> /label= Table 3	
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<220> <221> misc_feature <222> (1)..(22) <223> /label= Table 3	
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<210> 62 <211> 21	

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<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> /label= Table 3

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cagagtgtcc gagaggcagg g
21

<210> 63
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<220>
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<223> /label= Table 3

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<210> 64
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<212> DNA
<213> Homo sapiens

<220>
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<223> /label= Table 3

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<222> (1)..(20)
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<210> 66
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<221> misc_feature

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<222> (1)..(20)
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<210> 67
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<210> 68
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<222> (1)..(1302)
<223> /note= Flanking 5' genomic region of the sequence of the human nCL1 cDNA
described in Figure 2a

<220>
<221> misc_feature
<222> (-477)..(-472)
<223> /note= Putative Spl in Figure 2a

<220>
<221> misc_feature
<222> (-364)..(-343)
<223> /note= MEF2 binding sites in Figure 2a

<220>
<221> misc_feature
<222> (-685)..(-672)
<223> /note= CArG box in Figure 2a

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ttaagacgga gtctctttct gtcacctggg ctggagtgca gtggcgtgat ctgggttcac 180
tacaacctct cctccttggg ttcaagcaat tcttctgtct cagcctccca agtagctggg 240
attacaggca ccccccgcca caccggcctt atttttgtat ttttagtaga gacagggttt 300
cactattgtt gtccatgctg gtctcgaact cgtgacctca tgtgatccac ccgcctcggc 360
ctcccaaagt gcagagatta gagacgtgat ccacatggcc cagcaggacc acttttttagc 420
agattcagtc ccagtgttca ttttgtggat ggggagagac aagaggtggc aaggtcaagt 480
gtgcaggtag agacagggat tttctcaa atgaggactctg ctgagtagca ttttccatgc 540
agacatttcc aatgagcgct gacccaagaa cattctaaaa aagataccaa atctaacatt 600
gaataatgtt ctgatatcct aaaatttttag gactaaaaat catgttctct aaaattcaca 660

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gaatatTTTT gtagaattca gtacctcccg ttcaccctaa ctagctTTTT tgcaatattg 720
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tgtcagcagt tctcagcttc tttccagtgt tcaccttact cagatactcc cttttcattt 840
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<210> 69

<211> 1381

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(1381)

<223> /note= Flanking 3' genomic region of the sequence of the human nCL1 cDNA described in Figure 2c

<400> 69

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tttacctcaa aggacccagc agctacaccc ctacaggctt ccaggcacct catcagtcac 132
gttcctcctc catttttacc cctacccatc cttgatcggc catgcctagc ctgacccttt 192
agtaaagcaa tgaggtagga agaacaaacc cttgtccctt tgccatgtgg aggaaagtgc 252
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caccttcacg ctgtcccacc atggggccagg aaccaaacca gcaactgggtt ctactgctgt 432
ggggtaaact aactcagtgg aatagggctg gttactttgg gctgtccaac tcataagttt 492
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aataggagaa agattttcaa cagcttttcc tccttgacct cctcctttcc caattttatt 1332
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<210> 70

<211> 2466

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(2466)

<223> /note= Sequence of the human nCL1 cDNA described in Figure 2b

<400> 70

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atcagccgca attttcctat tatcggagtg aaagagaaga cattcgagca acttcacaag 198
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<210> 71

<211> 11

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> /label= Table 2

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